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RAW SEQUENCE LISTING   DATE: 10/03/2001
PATENT APPLICATION: **US/09/674,237A**   TIME: 08:24:49

Input Set : **A:\3477.89 Sequence Listing.txt**
Output Set: **N:\CRF3\10032001\I674237A.raw**

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 3 <110> APPLICANT: Egan, Sean E.
 4          Wang, Wei
 5          Sengar, Ameet
 7 <120> TITLE OF INVENTION: ESE GENES AND PROTEINS
 9 <130> FILE REFERENCE: 3477.89
11 <140> CURRENT APPLICATION NUMBER: US 09/674,237A
12 <141> CURRENT FILING DATE: 1999-04-27
14 <150> PRIOR APPLICATION NUMBER: PCT/CA99/00375
15 <151> PRIOR FILING DATE: 1999-04-27
17 <150> PRIOR APPLICATION NUMBER: US 60/118,739
18 <151> PRIOR FILING DATE: 1999-02-05
20 <150> PRIOR APPLICATION NUMBER: CA 2230201
21 <151> PRIOR FILING DATE: 1998-04-27
23 <160> NUMBER OF SEQ ID NOS: 33
25 <170> SOFTWARE: PatentIn version 3.1
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 93 tctagagagc taagaattgc tgaaatcacc cacttacagc agcagttgca ggaatctcag  1860
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221 Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe Leu Ser Leu
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224 aag ccg ata gcg gga ttt att act ggt gat caa gcg agg aac ttt ttt         144
225 Lys Pro Ile Ala Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe
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228 ttc caa tct ggg tta cct cag cct gtc tta gca caa ata tgg gcg cta         192
229 Phe Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu
230     50                  55                  60
232 gcg gac atg aat aac gat gga agg atg gat caa gtg gaa ttt tcc ata         240
233 Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Val Glu Phe Ser Ile
234 65                  70                  75                  80
236 gcc atg aag ctt atc aaa ctg aag cta caa gga tat cag ctc ccc tcc         288
237 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Gln Leu Pro Ser
238                 85                  90                  95
240 aca ctt ccc cct gtc atg aaa cag caa cca gtg gct att tcc agt gca         336
241 Thr Leu Pro Pro Val Met Lys Gln Gln Pro Val Ala Ile Ser Ser Ala
242             100                 105                 110
244 cca gca ttt ggt ata gga ggg att gct agc atg cca cca ctc aca gct         384
245 Pro Ala Phe Gly Ile Gly Gly Ile Ala Ser Met Pro Pro Leu Thr Ala
246         115                 120                 125
248 gtt gct cct gtg cca atg ggc tcc att cca gtt gtt gga atg tct cca         432
249 Val Ala Pro Val Pro Met Gly Ser Ile Pro Val Val Gly Met Ser Pro
250         130                 135                 140
252 ccc tta gta tct tct gtc cct cca gca gca gtg cct ccc ctg gct aac         480
253 Pro Leu Val Ser Ser Val Pro Pro Ala Ala Val Pro Pro Leu Ala Asn
254 145                 150                 155                 160
256 ggg gct cct ccc gtc ata cag cct ctg cct gcg ttt gcg cat cct gca         528
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PATENT APPLICATION: US/09/674,237A

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Input Set : A:\3477.89 Sequence Listing.txt
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261 Ala Thr Trp Pro Lys Ser Ser Ser Phe Ser Arg Ser Gly Pro Gly Ser
262              180             185             190
264 caa tta aac act aag tta cag aag gca caa tca ttc gat gtc gcc agc    624
265 Gln Leu Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Ala Ser
266          195             200             205
268 gcc cct cca gca gca gaa tgg gct gtg cct cag tca tca agg ctg aaa    672
269 Ala Pro Pro Ala Ala Glu Trp Ala Val Pro Gln Ser Ser Arg Leu Lys
270      210             215             220
272 tac agg cag tta ttc aac agc cac gac aaa act atg agt gga cac tta    720
273 Tyr Arg Gln Leu Phe Asn Ser His Asp Lys Thr Met Ser Gly His Leu
274 225             230             235             240
276 aca ggt ccc cag gca aga act att ctc atg caa tca agt tta ccc cag    768
277 Thr Gly Pro Gln Ala Arg Thr Ile Leu Met Gln Ser Ser Leu Pro Gln
278              245             250             255
280 gct cag ctg gct tca ata tgg aat ctt tct gac att gat caa gat gga    816
281 Ala Gln Leu Ala Ser Ile Trp Asn Leu Ser Asp Ile Asp Gln Asp Gly
282          260             265             270
284 aaa ctc act gca gaa gaa ttt atc cta gct atg cac cta att gat gtt    864
285 Lys Leu Thr Ala Glu Glu Phe Ile Leu Ala Met His Leu Ile Asp Val
286          275             280             285
288 gcc atg tct ggt cag cca ctg ccg ccc gtc ctg cct cca gaa tac atc    912
289 Ala Met Ser Gly Gln Pro Leu Pro Pro Val Leu Pro Pro Glu Tyr Ile
290      290             295             300
292 cct cct tcc ttc aga aga gtt cgc tcc ggc agt ggg atg tcc gtc ata    960
293 Pro Pro Ser Phe Arg Arg Val Arg Ser Gly Ser Gly Met Ser Val Ile
294 305             310             315             320
296 agc tct tct tct gtg gat cag agg ctg cct gag gag ccg tcg tca gag    1008
297 Ser Ser Ser Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Ser Ser Glu
298              325             330             335
300 gat gag cag cag cca gag aag aaa ctg cct gtg aca ttt gaa gat aag    1056
301 Asp Glu Gln Gln Pro Glu Lys Lys Leu Pro Val Thr Phe Glu Asp Lys
302          340             345             350
304 aag cgg gag aac ttc gag cga ggc agt gtg gag ctg gag aag cgc cgc    1104
305 Lys Arg Glu Asn Phe Glu Arg Gly Ser Val Glu Leu Glu Lys Arg Arg
306          355             360             365
308 caa gcg ctc ttg gag cag cag cgc aaa gag cag gag cgg ttg gct cag    1152
309 Gln Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala Gln
310      370             375             380
312 ctg gag cgc gcc gag cag gag agg aaa gag cgg gag cgc cag gag cag    1200
313 Leu Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Glu Gln
314 385             390             395             400
316 gag gcc aag cgg cag ctg gag ctg gag aag cag ctg gag aag cag cgg    1248
317 Glu Ala Lys Arg Gln Leu Glu Leu Glu Lys Gln Leu Glu Lys Gln Arg
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320 gag ctg gag cgg cag cga gag gag gag agg agg aag gag atc gag agg    1296
321 Glu Leu Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg
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328 gaa cgg aac cgg aga cag gaa ctc ctg aat cag agg aac aag gag cag     1392
329 Glu Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Lys Glu Gln
330          450                    455                   460
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333 Glu Gly Thr Val Val Leu Lys Ala Arg Arg Lys Thr Leu Glu Phe Glu
334 465                    470                   475                480
336 tta gaa gct ctg aat gac aaa aag cat cag cta gaa gga aaa ctt cag     1488
337 Leu Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu Gln
338              485                    490                   495
340 gat atc agg tgt cga ctg gca acc cag agg caa gaa att gag agc acg     1536
341 Asp Ile Arg Cys Arg Leu Ala Thr Gln Arg Gln Glu Ile Glu Ser Thr
342          500                    505                   510
344 aac aag tct aga gag cta aga att gct gaa atc acc cac tta cag cag     1584
345 Asn Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln Gln
346          515                    520                   525
348 cag ttg cag gaa tct cag caa atg ctt gga aga ctt att cca gag aaa     1632
349 Gln Leu Gln Glu Ser Gln Gln Met Leu Gly Arg Leu Ile Pro Glu Lys
350          530                    535                   540
352 cag ata ctc agt gac cag tta aaa caa gtc cag cag aac agt ttg cat     1680
353 Gln Ile Leu Ser Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu His
354 545                    550                   555                560
356 aga gac tcg ctt ctt acc ctc aaa aga gcc ttg gaa gca aag gag ctg     1728
357 Arg Asp Ser Leu Leu Thr Leu Lys Arg Ala Leu Glu Ala Lys Glu Leu
358              565                    570                   575
360 gcc cgg cag cag ctc cgg gag cag ctg gac gag gtg gag aga gag acc     1776
361 Ala Arg Gln Gln Leu Arg Glu Gln Leu Asp Glu Val Glu Arg Glu Thr
362          580                    585                   590
364 agg tca aag ctg cag gag att gat gtt ttc aac aac cag ctg aag gaa     1824
365 Arg Ser Lys Leu Gln Glu Ile Asp Val Phe Asn Asn Gln Leu Lys Glu
366          595                    600                   605
368 ctg aga gag ata cat agc aaa cag caa ctc cag aag cag agg tcc ctg     1872
369 Leu Arg Glu Ile His Ser Lys Gln Gln Leu Gln Lys Gln Arg Ser Leu
370 610                    615                   620
372 gag gca gcg cga ctg aag cag aaa gag cag gag agg aag agc ctg gag     1920
373 Glu Ala Ala Arg Leu Lys Gln Lys Glu Gln Glu Arg Lys Ser Leu Glu
374 625                    630                   635                640
376 tta gag aag caa aag gaa gac gct cag aga cga gtt cag gaa agg gac     1968
377 Leu Glu Lys Gln Lys Glu Asp Ala Gln Arg Arg Val Gln Glu Arg Asp
378              645                    650                   655
380 aag caa tgg ctg gag cat gtg cag cag gag gag cag cca cgc ccc cgg     2016
381 Lys Gln Trp Leu Glu His Val Gln Gln Glu Glu Gln Pro Arg Pro Arg
382              660                    665                   670
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385 Lys Pro His Glu Glu Asp Arg Leu Lys Arg Glu Asp Ser Val Arg Lys
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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
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